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gaa 2043

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<210> 8
<211> 501
<212> PRT
<213> Mus musculus

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<400> 8

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Leu Pro Ala Gln Gly Thr His Leu Gly Ile Arg Leu Pro Leu Arg Ser
20           25           30

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Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
35           40           45

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Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
50           55           60

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```

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
65           70           75           80

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Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
85           90           95

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Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
100          105          110

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Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
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Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Ile Pro  
195 200 205

Asn Ile Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220

Thr Glu Ala Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Val Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Ala Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala  
450 455 460

Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp  
465 470 475 480

Arg Cys Leu Arg Cys Leu Arg His Gln His Asp Asp Phe Ala Asp Asp  
485 490 495

Ile Ser Leu Leu Lys  
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<210> 9  
<211> 2088  
<212> DNA  
<213> Homo sapiens

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggaccaa 180  
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gtggaggttg acgccgtgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040
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<210> 10  
 <211> 695  
 <212> PRT  
 <213> Homo sapiens

<400> 10

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln					
	35		40		45
Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp					
	50		55		60
Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu					
	65		70		75
Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn					
		85		90	95
Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val					
		100		105	110
Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu					
		115		120	125
Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys					
		130		135	140
Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu					
		145		150	155
Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile					
		165		170	175
Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu					
		180		185	190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val					
		195		200	205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys					
		210		215	220
Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu					
		225		230	235
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu					
		245		250	255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile					
		260		265	270



Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

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<212> DNA  
<213> Homo sapiens

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ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt 360  
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gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg	660
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<210> 12  
 <211> 695  
 <212> PRT  
 <213> Homo sapiens

<400> 12

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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

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<211> 2088

<212> DNA

<213> Homo sapiens

<400> 13

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ggctacgaaa atccaaccta caagttcttt gagcagatgc agaactag 2088

<210> 14

<211> 695

<212> PRT

<213> Homo sapiens

<400> 14

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20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu



245	250	255
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile 260 265 270		
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg 275 280 285		
Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu 290 295 300		
Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys 305 310 315 320		
Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg 325 330 335		
Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp 340 345 350		
Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu 355 360 365		
Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala 370 375 380		
Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn 385 390 395 400		
Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe 405 410 415		
Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His 420 425 430		
Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala 435 440 445		
Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu 450 455 460		
Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala 465 470 475 480		
Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn 485 490 495		

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn  
690 695

<210> 15  
<211> 2094  
<212> DNA  
<213> Homo sapiens

<400> 15  
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cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatgtt ctgtggcaga 120  
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacacaaa 180

acctgcattg	ataccaagga	aggcatcctg	cagtattgcc	aagaagtcta	ccctgaactg	240
cagatcacca	atgtggtaga	agccaaccaa	ccagtgacca	tccagaactg	gtgcaagcgg	300
ggccgcaagc	agtgaagac	ccatccccac	tttgtgattc	cctaccgctg	cttagttggt	360
gagtttgtaa	gtgatgccct	tctcgttcct	gacaagtgca	aattcttaca	ccaggagagg	420
atggatgttt	gcgaaactca	tcttctactg	cacaccgtcg	ccaaagagac	atgcagtgag	480
aagagtacca	acttgcatga	ctacggcatg	ttgtgtccct	gcggaattga	caagttccga	540
ggggtagagt	ttgtgtgttg	cccactggct	gaagaaagtg	acaatgtgga	ttctgtgat	600
gcggaggagg	atgactcgga	tgtctggtgg	ggcggagcag	acacagacta	tgcagatggg	660
agtgaagaca	aagtagtaga	agtagcagag	gaggaagaag	tggctgaggt	ggaagaagaa	720
gaagccgatg	atgacgagga	cgatgaggat	ggtgatgagg	tagaggaaga	ggctgaggaa	780
ccctacgaag	aagccacaga	gagaaccacc	agcattgcc	ccaccaccac	caccaccaca	840
gagtctgtgg	aagaggtgg	tcgagttcct	acaacagcag	ccagtacccc	tgatgccgtt	900
gacaagtatc	tcgagacacc	tggggatgag	aatgaacatg	cccatttcca	gaaagccaaa	960
gagaggcttg	aggccaagca	ccgagagaga	atgtcccagg	tcatgagaga	atgggaagag	1020
gcagaacgtc	aagcaaagaa	cttgccataa	gctgataaga	aggcagttat	ccagcatttc	1080
caggagaaag	tggaatcttt	ggaacaggaa	gcagccaacg	agagacagca	gctggtggag	1140
acacacatgg	ccagagtgg	agccatgctc	aatgaccgcc	gccgcctggc	cctggagaac	1200
tacatcaccc	ctctgcaggc	tgttcctcct	cggcctcgtc	acgtgttcaa	tatgctaaag	1260
aagtatgtcc	gcgcagaaca	gaaggacaga	cagcacaccc	taaagcattt	cgagcatgtg	1320
cgcattggtg	atcccaagaa	agccgctcag	atccggtccc	aggttatgac	acacctccgt	1380
gtgatttatg	agcgcataaa	tcagtctctc	tccctgctct	acaacgtgcc	tgcagtggcc	1440
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gtcttgggca	acatgattag	tgaaccaagg	atcagttacg	gaaacgatgc	tctcatgcc	1560
tctttgaccg	aaacgaaaac	caccgtggag	ctccttccc	tgaatggaga	gttcagcctg	1620
gacgatctcc	agccgtggca	ttcttttggg	gctgactctg	tgccagccaa	cacagaaaac	1680
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cgacatgact	caggatatga	agttcatcat	caaaaattgg	tgttctttgc	agaagatgtg	1860
ggttcaaaca	aaggtgcaat	cattggactc	atggtggg	gtgttgatc	agcgacagt	1920
atcgatcatc	ccttggtgat	gctgaagaag	aaacagtaca	catccattca	tcatggtgtg	1980
gtggagggtg	acgccgctgt	caccccagag	gagcgccacc	tgtccaagat	gcagcagaac	2040
ggctacgaaa	atccaacct	caagttcttt	gagcagatgc	agaacaagaa	gtag	2094

<210> 16  
<211> 697  
<212> PRT  
<213> Homo sapiens

<400> 16  
Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	225	230	235	240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	245	250	255	
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	260	265	270	
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	275	280	285	
Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	290	295	300	
Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	305	310	315	320
Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	325	330	335	
Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	340	345	350	
Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	355	360	365	
Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	370	375	380	
Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	385	390	395	400
Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	405	410	415	
Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	420	425	430	
Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	435	440	445	
Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	450	455	460	
Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	465	470	475	480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

<210> 17  
<211> 2094  
<212> DNA  
<213> Homo sapiens

<400> 17  
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cccactgatg gtaatgctgg cctgctggct gaaccccaga ttgccatggt ctgtggcaga	120
ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacccaaa	180
acctgcattg ataccaagga aggcattcctg cagtattgcc aagaagtcta cctgaactg	240
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg	300
ggccgcaagc agtgcaagac ccatcccccac tttgtgattc cctaccgctg cttagtgtgt	360
gagtttgtaa gtgatgccct tctcgttcct gacaagtgc aattcttaca ccaggagagg	420
atggatgttt gcgaaactca tcttcactgg cacaccgtcg ccaaagagac atgcagtgag	480
aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga	540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat	600
gcggaggagg atgactcgga tgtctggtgg ggcggagcag acacagacta tgcagatggg	660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa	720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa	780
ccctacgaag aagccacaga gagaaccacc agcattgcc aaccaccac caccaccaca	840
gagtctgtgg aagagggtgt tcgagttcct acaacagcag ccagtacccc tgatgccgtt	900
gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa	960
gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag	1020
gcagaacgtc aagcaaagaa cttgcctaaa gctgataaga aggcagttat ccagcatttc	1080
caggagaaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctgggtggag	1140
acacacatgg ccagagtgga agccatgctc aatgaccgcc gccgcctggc cctggagaac	1200
tacatcaccg ctctgcaggc tgttctcct cggcctcgtc acgtgttcaa tatgctaaag	1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacacc taaagcattt cgagcatgtg	1320
cgcattggtg atcccaagaa agccgctcag atccggtccc aggttatgac acacctccgt	1380
gtgatttatg agcgcattga tcagtctctc tccctgctct acaacgtgcc tgcagtggcc	1440
gaggagattc aggatgaagt tgatgagctg cttcagaaa agcaaaaacta ttcagatgac	1500
gtcttgccca acatgattag tgaaccaagg atcagttacg gaaacgatgc tctcatgcca	1560
tctttgaccg aaacgaaaac caccgtggag ctccctcccc tgaatggaga gttcagcctg	1620
gacgatctcc agccgtggca ttcttttggg gctgactctg tgccagccaa cacagaaaac	1680
gaagttgagc ctgttgatgc ccgccctgct gccgaccgag gactgaccac tcgaccagg	1740
tctgggttga caaatatcaa gacggaggag atctctgaag tgaatctgga tgcagaattc	1800
cgacatgact caggatatga agttcatcat caaaaattgg tgttctttgc agaagatgtg	1860
ggttcaaaca aagtgcaat cattggactc atggtgggcg gtgtgtcat agcgacagt	1920
atcgatcatc ccttggtgat gctgaagaag aaacagtaca catccattca tcatggtgtg	1980

gtggagggttg acgccgctgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040

ggctacgaaa atccaaccta caagttcttt gagcagatgc agaacaagaa gtag 2094

<210> 18

<211> 697

<212> PRT

<213> Homo sapiens

<400> 18

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205



Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu  
290 295 300

Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys  
305 310 315 320

Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg  
325 330 335

Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp  
340 345 350

Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu  
355 360 365

Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala  
370 375 380

Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn  
385 390 395 400

Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe  
405 410 415

Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His  
420 425 430

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Asn Leu Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

<210> 19  
<211> 2094  
<212> DNA

<213> Homo sapiens

<400> 19

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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacccaaa	180
acctgcattg ataccaagga aggcatactg cagtattgcc aagaagtcta ccctgaactg	240
cagatcacca atgtggtaga agccaaccaa ccagtgacca tccagaactg gtgcaagcgg	300
ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttagt	360
gagtttgtaa gtgatgccct tctcgttctt gacaagtgca aattcttaca ccaggagagg	420
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aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga	540
ggggtagagt ttgtgtgttg cccactggct gaagaaagtg acaatgtgga ttctgctgat	600
gcggaggagg atgactcgga tgtctggtgg ggccggagcag acacagacta tgcagatggg	660
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa	720
gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa	780
ccctacgaag aagccacaga gagaaccacc agcattgcc aaccaccac caccaccaca	840
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gacaagtatc tcgagacacc tggggatgag aatgaacatg cccatttcca gaaagccaaa	960
gagaggcttg aggccaagca ccgagagaga atgtcccagg tcatgagaga atgggaagag	1020
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caggagaaaag tggaatcttt ggaacaggaa gcagccaacg agagacagca gctggtggag	1140
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tacatcaccg ctctgcaggc tgttcctcct cggcctcgtc acgtgttcaa tatgctaaag	1260
aagtatgtcc gcgcagaaca gaaggacaga cagcacaccc taaagcattt cgagcatgtg	1320
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tctgggttga caaatatcaa gacggaggag atctctgaag tgaagatgga tgcagaattc	1800

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 atcttcatca ccttgggtgat gctgaagaag aaacagtaca catccattca tcatgggtgtg 1980  
 gtggaggttg acgcccgtgt caccacagag gagcgccacc tgtccaagat gcagcagaac 2040  
 ggctacgaaa atccaadcta caagttcttt gagcagatgc agaacaagaa gtag 2094

<210> 20  
 <211> 697  
 <212> PRT  
 <213> Homo sapiens

<400> 20

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
 20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
 100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
 115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
 130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
 145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
 165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu

180	185	190
Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val 195 200 205		
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys 210 215 220		
Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu 225 230 235 240		
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu 245 250 255		
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile 260 265 270		
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg 275 280 285		
Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu 290 295 300		
Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys 305 310 315 320		
Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg 325 330 335		
Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp 340 345 350		
Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu 355 360 365		
Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala 370 375 380		
Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn 385 390 395 400		
Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe 405 410 415		
Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His 420 425 430		

Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala  
435 440 445

Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu  
450 455 460

Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala  
465 470 475 480

Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn  
485 490 495

Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510

Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525

Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540

Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560

Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575

Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590

Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605

His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620

Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val  
625 630 635 640

Ile Phe Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile  
645 650 655

His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670

His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685

Phe Phe Glu Gln Met Gln Asn Lys Lys  
690 695

<210> 21  
<211> 1341  
<212> DNA  
<213> Homo sapiens

<400> 21  
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gacgaagagc ccgaggagcc cggccggagg ggcagctttg tggagatggt ggacaacctg 180  
aggggcaagt cggggcaggg ctactacgtg gagatgaccg tgggcagccc cccgcagacg 240  
ctcaacatcc tgggtggatac aggcagcagt aactttgcag tgggtgctgc cccccacccc 300  
ttcctgcacg gctactacca gaggcagctg tccagcacat accgggacct ccggaagggg 360  
gtgtatgtgc cctacacca gggcaagtgg gaaggggagc tgggcaccga cctggtaagc 420  
atcccccatg gcccacacgt cactgtgcgt gccaacattg ctgccatcac tgaatcagac 480  
aagttcttca tcaacggctc caactgggaa ggcacacctg ggctggccta tgetgagatt 540  
gccaggcctg acgactccct ggagcctttc tttgactctc tggtaaagca gaccacggtt 600  
cccaacctct tctccctgca cctttgtggg gctggcttcc ccctcaacca gtctgaagtg 660  
ctggcctctg tcggaggagg catgatcatt ggaggtatcg accactcgct gtacacaggc 720  
agtctctggt atacacccat ccggcgggag tggattatg aggtcatcat tgtgcgggtg 780  
gagatcaatg gacaggatct gaaaatggac tgcaaggagt acaactatga caagagcatt 840  
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tccatcaagg cagcctctc cacggagaag ttcctgatg gtttctggct aggagagcag 960  
ctggtgtgct ggcaagcagg caccacccct tggaacattt tcccagtcac ctactctac 1020  
ctaattgggtg aggttaccaa ccagtccttc cgcacacca tccttcgca gcaataacctg 1080  
cggccagtgg aagatgtggc cagtcacca gacgactgtt acaagtttgc catctcacag 1140  
tcatccacgg gcaactgtat gggagctgtt atcatggagg gcttctacgt tgtctttgat 1200  
cgggcccga aacgaattgg ctttgcgtgc agcgttgcc atgtgcacga tgagttcagg 1260  
acggcagcgg tggaaggccc tttgtcacc ttggacatgg aagactgtgg ctacaacatt 1320  
ccacagacag atgagtcag a 1341

<210> 22  
<211> 446

<212> PRT

<213> Homo sapiens

<400> 22

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Thr Gln  
1 5 10 15

His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu  
20 25 30

Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly  
35 40 45

Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser  
50 55 60

Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr  
65 70 75 80

Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala  
85 90 95

Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser  
100 105 110

Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly  
115 120 125

Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly  
130 135 140

Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp  
145 150 155 160

Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala  
165 170 175

Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp  
180 185 190

Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu  
195 200 205

Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val  
210 215 220

Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly  
225 230 235 240



Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile  
245 250 255

Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys  
260 265 270

Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu  
275 280 285

Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala  
290 295 300

Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln  
305 310 315 320

Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val  
325 330 335

Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile  
340 345 350

Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr  
355 360 365

Ser Gln Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly  
370 375 380

Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp  
385 390 395 400

Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His  
405 410 415

Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp  
420 425 430

Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
435 440 445

<210> 23

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 23

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ccgcgtgaac aggacggatc caccacagcac ggcacccggc tgcccctgcg cagcggcctg 120

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gggggcgccc ccctggggct gcggtgccc cgggagaccg acgaagagcc cgaggagccc 180
ggccggaggg gcagctttgt ggagatggtg gacaacctga ggggcaagtc ggggcagggc 240
tactacgtgg agatgaccgt gggcagcccc ccgcagacgc tcaacatcct ggtggataca 300
ggcagcagta actttgcagt ggggtgctgcc cccacccct tcctgcatcg ctactaccag 360
aggcagctgt ccagcacata ccgggacctc cggaaggggtg tgtatgtgcc ctacacccag 420
ggcaagtggg aaggggagct gggcacccgac ctggtaagca tccccatgg cccaacgtc 480
actgtgcgtg ccaacattgc tgccatcact gaatcagaca agttcttcat caacggctcc 540
aactgggaag gcatcctggg gctggcctat gctgagattg ccaggcctga cgactccctg 600
gagcctttct ttgactctct ggtaaagcag acccacgttc ccaacctctt ctccctgcac 660
ctttgtggtg ctggcttccc cctcaaccag tctgaagtgc tggcctctgt cggagggagc 720
atgatcattg gaggtatcga ccactcgctg tacacaggca gtctctggta tacacccatc 780
cggcgggagt ggtattatga ggtcatcatt gtgcgggtgg agatcaatgg acaggatctg 840
aaaatggact gcaaggagta caactatgac aagagcattg tggacagtgg caccaccaac 900
cttcgtttgc ccaagaaaagt gtttgaagct gcagtcaaat ccatcaaggc agcctcctcc 960
acggagaagt tccctgatgg tttctggcta ggagagcagc tgggtgtgctg gcaagcaggc 1020
accacccctt ggaacatttt ccagtcac tcactctacc taatgggtga ggttaccac 1080
cagtccttcc gcatcaccat ccttcgcag caatacctgc ggccagtgga agatgtggcc 1140
acgtcccaag acgactgtta caagtttgc atctcacagt catccacggg cactgttatg 1200
ggagctgtta tcatggaggg cttctacgtt gtctttgatc gggccgaaa acgaattggc 1260
tttgctgtca gcgcttgcca tgtgcacgat gagttcagga cggcagcggg ggaaggccct 1320
tttgtcacct tggacatgga agactgtggc tacaacattc cacagacaga tgagtcatga 1380

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```

<210> 24
<211> 459
<212> PRT
<213> Homo sapiens

```

<400> 24

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Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr
1           5           10          15

```

```

Ile Ser Asp Ser Pro Arg Glu Gln Asp Gly Ser Thr Gln His Gly Ile
20           25          30

```

```

Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg
35           40          45

```

```

Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly

```

50	55	60
Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly		
65	70	75 80
Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile		
	85	90 95
Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His		
	100	105 110
Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg		
	115	120 125
Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu		
	130	135 140
Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val		
145	150	155 160
Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe		
	165	170 175
Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu		
	180	185 190
Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val		
	195	200 205
Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala		
	210	215 220
Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser		
225	230	235 240
Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp		
	245	250 255
Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg		
	260	265 270
Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn		
	275	280 285
Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro		
	290	295 300

Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser  
305 310 315 320

Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys  
325 330 335

Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu  
340 345 350

Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu  
355 360 365

Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp  
370 375 380

Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met  
385 390 395 400

Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg  
405 410 415

Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe  
420 425 430

Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp  
435 440 445

Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
450 455

<210> 25

<211> 1302

<212> DNA

<213> Homo sapiens

<400> 25

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gtggagatgg tggacaacct gaggggcaag tcggggcagg gctactacgt ggagatgacc 180

gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 240

gtgggtgctg cccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 300

taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 360

ctgggcaccg acctggtaag catcccccat ggcccacg tcaactgtgc tgccaacatt 420

gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacacct 480

gggctggcct atgctgagat tgccaggcct gacgactccc tggagccttt ctttgactct 540

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ctggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggettc 600
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gaccactcgc tgtacacagg cagtctctgg tatacaccca tccggcgga gtggtattat 720
gaggtcatca ttgtgcgggt ggagatcaat ggacaggatc tgaaaatgga ctgcaaggag 780
tacaactatg acaagagcat tgtggacagt ggcaccacca accttcgttt gcccaagaaa 840
gtgtttgaag ctgcagtcaa atccatcaag gcagcctcct ccacggagaa gttccctgat 900
ggtttctggc taggagagca gctggtgtgc tggcaagcag gcaccacccc ttggaacatt 960
ttcccagtca tctcactcta cctaattgggt gaggttacca accagtcctt ccgcatcacc 1020
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tacaagtttg ccatctcaca gtcattccag ggcactgtta tgggagctgt tatcatggag 1140
ggcttctacg ttgtctttga tcgggcccga aaacgaattg gctttgctgt cagcgcttgc 1200
catgtgcacg atgagttcag gacggcagcg gtggaaggcc cttttgtcac cttggacatg 1260
gaagactgtg gctacaacat tccacagaca gatgagtcat ga 1302

```

```

<210> 26
<211> 433
<212> PRT
<213> Homo sapiens

```

```

<400> 26

```

```

Met Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly
1          5          10          15

```

```

Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu
          20          25          30

```

```

Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg
          35          40          45

```

```

Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro
          50          55          60

```

```

Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala
65          70          75          80

```

```

Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln
          85          90          95

```

```

Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr
          100          105          110

```

```

Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile

```

115						120						125			
Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr
130						135					140				
Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu
145					150					155					160
Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro
				165					170					175	
Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser
			180					185					190		
Leu	His	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu
		195					200					205			
Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu
	210					215					220				
Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr
225					230					235					240
Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met
				245					250					255	
Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr
			260					265					270		
Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser
		275					280					285			
Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu
	290					295					300				
Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile
305					310					315					320
Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser
				325					330					335	
Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp
			340					345					350		
Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser
		355					360					365			

Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val  
370 375 380

Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys  
385 390 395 400

His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val  
405 410 415

Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu  
420 425 430

Ser

<210> 27  
<211> 1278  
<212> DNA  
<213> Homo sapiens

<400> 27  
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ggcaagtcgg ggcagggcta ctacgtggag atgaccgtgg gcagcccccc gcagacgctc 180  
aacatcctgg tggatacagg cagcagtaac ttgacgtgg gtgctgcccc ccacctcttc 240  
ctgcatcgct actaccagag gcagctgtcc agcacatacc gggacctccg gaaggggtgtg 300  
tatgtgccct acaccaggga caagtgggaa ggggagctgg gcaccgacct ggtaagcatc 360  
ccccatggcc ccaacgtcac tgtgcgtgcc aacattgctg ccatcactga atcagacaag 420  
ttcttcatca acggctccaa ctgggaaggc atcctggggc tggcctatgc tgagattgcc 480  
aggcctgacg actccctgga gcctttcttt gactctctgg taaagcagac ccacgttccc 540  
aacctcttct ccctgcacct ttgtggtgct ggcttcccc tcaaccagtc tgaagtgtgtg 600  
gcctctgtcg gagggagcat gatcattgga ggtatcgacc actcgctgta cacaggcagt 660  
ctctggtata caccatccg gcgggagtggt tattatgagg tcatcattgt gcgggtggag 720  
atcaatggac aggatctgaa aatggactgc aaggagtaca actatgacaa gagcattgtg 780  
gacagtggca ccaccaacct tcgtttgccc aagaaagtgt ttgaagctgc agtcaaatcc 840  
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gcccgaaaac gaattggctt tgctgtcagc gcttgccatg tgcacgatga gttcaggacg 1200  
gcagcgggtgg aaggcccttt tgtcaccttg gacatggaag actgtggcta caacattcca 1260  
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<210> 28  
<211> 425  
<212> PRT  
<213> Homo sapiens

<400> 28

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Gly Ser Met Thr  
1 5 10 15

Ile Ser Asp Ser Pro Leu Asp Ser Gly Ile Glu Thr Asp Gly Ser Phe  
20 25 30

Val Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr  
35 40 45

Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val  
50 55 60

Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe  
65 70 75 80

Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu  
85 90 95

Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu  
100 105 110

Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val  
115 120 125

Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn  
130 135 140

Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala  
145 150 155 160

Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln  
165 170 175

Thr His Val Pro Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe  
180 185 190

Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile



195	200	205
Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr 210 215 220		
Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu 225 230 235 240		
Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp 245 250 255		
Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys 260 265 270		
Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu 275 280 285		
Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln 290 295 300		
Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu 305 310 315 320		
Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln 325 330 335		
Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys 340 345 350		
Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala 355 360 365		
Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg 370 375 380		
Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr 385 390 395 400		
Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly 405 410 415		
Tyr Asn Ile Pro Gln Thr Asp Glu Ser 420 425		

<210> 29  
 <211> 1362  
 <212> DNA

<213> Homo sapiens

<400> 29

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<210> 30

<211> 453

<212> PRT

<213> Homo sapiens

<400> 30

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1           5           10          15
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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
20          25          30
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Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp	35	40	45	
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val	50	55	60	
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr	65	70	75	80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser	85	90	95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr	100	105	110	
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	115	120	125	
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	130	135	140	
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	145	150	155	160
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	165	170	175	
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	180	185	190	
Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	195	200	205	
Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	210	215	220	
Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	225	230	235	240
Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	245	250	255	
Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	260	265	270	
Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	275	280	285	

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser  
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<210> 31  
<211> 1380  
<212> DNA  
<213> Homo sapiens

<400> 31  
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ctggtaaagc agaccacagt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660  
cccccaacc agtctgaagt gctggcctct gtcggaggga gcatgatcat tggaggatc 720  
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<210> 32  
<211> 459  
<212> PRT  
<213> Homo sapiens

<400> 32

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
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Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp  
180 185 190

Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro  
195 200 205

Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln  
210 215 220

Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile  
225 230 235 240

Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg  
245 250 255

Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln  
260 265 270

Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val  
275 280 285

Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala  
290 295 300

Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp  
305 310 315 320

Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr  
325 330 335

Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val  
340 345 350

Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg  
355 360 365

Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala  
370 375 380

Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu  
385 390 395 400

Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala  
405 410 415

Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu  
420 425 430

Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro  
435 440 445

Gln Thr Asp Glu Ser His His His His His His  
450 455

<210> 33  
<211> 25  
<212> PRT  
<213> Homo sapiens

<400> 33

Ser Glu Gln Gln Arg Arg Pro Arg Asp Pro Glu Val Val Asn Asp Glu  
1 5 10 15

Ser Ser Leu Val Arg His Arg Trp Lys  
20 25

<210> 34  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 34

Ser Glu Gln Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp Ile Ser  
1 5 10 15

Leu Leu Lys

<210> 35  
<211> 29  
<212> DNA  
<213> Homo sapiens

<400> 35

gtggatccac ccagcacggc atccggctg 29

<210> 36  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 36  
gaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 37  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 37  
gatcgatgac tatctctgac tctccgctg aacaggacg 39

<210> 38  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 38  
gatccgtcct gttcacgcgg agagtcagag atagtcac 39

<210> 39  
<211> 77  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Hu-Asp2

<400> 39  
cggcatccgg ctgcccctgc gtagcgggtct ggggtgggtgct ccactggggtc tgcgtctgcc 60  
ccgggagacc gacgaag 77

<210> 40  
<211> 77  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Hu-Asp2

<400> 40  
cttcgtcggg ctcccggggc agacgcagac ccagtggagc accacccaga ccgctacgca 60  
ggggcagccg gatgccg 77

<210> 41  
<211> 51  
<212> DNA  
<213> Caspase-8 Cleavage Site



<400> 41  
gatcgaatgac tatctctgac tctccgctgg actctggtat cgaaaccgac g 51

<210> 42  
<211> 51  
<212> DNA  
<213> Caspase-8 Cleavage Site

<400> 42  
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<210> 43  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 43  
aaggatcctt tgtggagatg gtggacaacc tg 32

<210> 44  
<211> 36  
<212> DNA  
<213> Homo sapiens

<400> 44  
gaaagctttc atgactcatc tgtctgtgga atgttg 36

<210> 45  
<211> 24  
<212> DNA  
<213> 6-His tag

<400> 45  
gatcgatca tcaccatcac catg 24

<210> 46  
<211> 24  
<212> DNA  
<213> 6-His tag

<400> 46  
gatccatggt gatggtgatg atgc 24

<210> 47  
<211> 22  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer

<400> 47  
gactgaccac tcgaccaggt tc 22

<210> 48

<211> 51  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer

<400> 48  
cgaattaaat tccagcacac tggctacttc ttgttctgca tctcaaagaa c 51

<210> 49  
<211> 26  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Primer

<400> 49  
cgaattaaat tccagcacac tggcta 26

<210> 50  
<211> 1287  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Hu-Asp2(b) delta TM

<400> 50  
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ctgcggctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180  
gtggagatgg tggacaacct gaggggcaag tgggggcagg gctactacgt ggagatgacc 240  
gtgggcagcc ccccgagac gctcaacatc ctggtggata caggcagcag taactttgca 300  
gtgggtgctg ccccccaccc ctctctgcat cgctactacc agaggcagct gtccagcaca 360  
taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgc tgccaacatt 480  
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcacctg 540  
gggctggcct atgtgagat tgccaggctt tgtgggtgctg gcttccccct caaccagtct 600  
gaagtgtctg cctctgtcgg agggagcatg atcattggag gtatcgacca ctgctgtac 660  
acaggcagtc tctggtatac acccatccgg cgggagtggt attatgaggt catcattgtg 720  
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ctctacctaa tgggtgaggt taccaaccag tccttcgca tcaccatcct tccgcagcaa 1020  
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 tcacagtcac ccacgggcac tggtatggga gctgttatca tggagggctt ctacgttgtc 1140  
 tttgatcggg cccgaaaacg aattggcttt gctgtcagcg cttgccatgt gcacgatgag 1200  
 ttcaggacgg cagcggtgga aggccctttt gtcaccttgg acatggaaga ctgtggctac 1260  
 aacattccac agacagatga gtcatga 1287

<210> 51  
 <211> 428  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> Hu-Asp2(b) delta TM

<400> 51

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
 20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
 35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
 50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
 65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
 85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
 100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
 115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
 130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
 145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly  
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser  
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile  
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser  
420 425

<210> 52  
<211> 1305  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Hu-Asp2(b) delta TM

<400> 52  
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ctgcggtctgc cccgggagac cgacgaagag cccgaggagc ccggccggag gggcagcttt 180  
gtggagatgg tggacaacct gaggggcaag tgggggcagg gctactacgt ggagatgacc 240  
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taccgggacc tccggaaggg tgtgtatgtg ccctacaccc agggcaagtg ggaaggggag 420  
ctgggcaccg acctggtaag catcccccat ggccccaacg tcaactgtgcg tgccaacatt 480  
gctgccatca ctgaatcaga caagttcttc atcaacggct ccaactggga aggcattcctg 540  
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aacattccac agacagatga gtcacagcag cagcagcagc agtga 1305

<210> 53  
<211> 434  
<212> PRT

<213> Artificial sequence

<220>

<223> Hu-Asp2(b) delta TM

<400> 53

Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
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Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30

Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45

Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60

Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80

Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95

Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110

Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125

Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140

Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
145 150 155 160

Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp  
165 170 175

Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Leu Cys Gly  
180 185 190

Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
195 200 205

Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
210 215 220

Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
225 230 235 240

Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
245 250 255

Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
260 265 270

Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
275 280 285

Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
290 295 300

Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser  
305 310 315 320

Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile  
325 330 335

Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
340 345 350

Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
355 360 365

Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
370 375 380

Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
385 390 395 400

Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
405 410 415

Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu Ser His His His His  
420 425 430

His His

<210> 54

<211> 2310

<212> DNA

<213> Homo sapiens

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<212> PRT  
<213> Homo sapiens

<400> 55

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
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Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
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Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
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Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
370 375 380

Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
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Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

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ggccgcaagc agtgcaagac ccatccccac tttgtgattc cctaccgctg cttagttggt 360  
gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg 420  
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gaagccgatg atgacgagga cgatgaggat ggtgatgagg tagaggaaga ggctgaggaa 780  
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cgagcaatga tctcccgctg gtactttgat gtgactgaag ggaagtgtgc cccattcttt 960  
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<210> 57
<211> 751
<212> PRT
<213> Homo sapiens

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<400> 57

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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20           25           30

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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35           40           45

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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp

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50

55

60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
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Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
				325					330					335	
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Ile	Pro	Thr	Thr	Ala	Ala	Ser	Thr
			340					345						350	
Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu
		355					360					365			
His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	Lys	His	Arg
	370					375					380				
Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln
385					390					395					400
Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	Gln	His	Phe
				405					410					415	
Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln
			420					425					430		
Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	Leu	Asn	Asp
		435					440					445			
Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val
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Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg
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Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	Glu	His	Val
				485					490					495	
Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	Gln	Val	Met
			500					505					510		
Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu
		515					520					525			
Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp
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Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	Tyr	Ser	Asp	Asp	Val	Leu	Ala	Asn
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Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro  
565 570 575

Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly  
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp  
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg  
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr  
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe  
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe  
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val  
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu  
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp  
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn  
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn  
740 745 750

<210> 58  
<211> 2316  
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acctacaagt tctttgagca gatgcagaac aagaag 2316

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<212> PRT  
<213> Homo sapiens

<400> 59

Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val

195	200	205
Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys		
210	215	220
Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu		
225	230	235
Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu		
	245	250
Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile		
	260	265
Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg		
	275	280
Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile		
290	295	300
Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe		
305	310	315
Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr		
	325	330
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr		
	340	345
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala		
355	360	365
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp		
370	375	380
Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala		
385	390	395
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala		
	405	410
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile		
	420	425
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn		
435	440	445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn Lys Lys  
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ctgaacatgc acatgaatgt ccagaatggg aagtgggatt cagatccatc agggacccaaa 180  
acctgcattg ataccaagga aggcatactg cagtattgcc aagaagtcta ccctgaactg 240  
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gagtttgtaa gtgatgccct tctcgttcct gacaagtgca aattcttaca ccaggagagg 420  
atggatgttt gcgaaactca tcttcaactgg cacaccgtcg ccaaagagac atgcagtgag 480  
aagagtacca acttgcatga ctacggcatg ttgctgccct gcggaattga caagttccga 540  
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gcggaggagg atgactcgga tgtctggtgg ggccggagcag acacagacta tgcagatggg 660  
agtgaagaca aagtagtaga agtagcagag gaggaagaag tggctgaggt ggaagaagaa 720  
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gagtctgtgg aagaggtggt tcgagaggtg tgctctgaac aagccgagac ggggccgtgc 900  
cgagcaatga tctcccgtg gtactttgat gtgactgaag ggaagtgtgc cccattcttt 960  
tacggcggat gtggcggcaa ccggaacaac tttgacacag aagagtactg catggccgtg 1020  
tgtggcagcg ccattcctac aacagcagcc agtaccctg atgccgttga caagtatctc 1080  
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 gaatctttgg aacaggaagc agccaacgag agacagcagc tggaggagac acacatggcc 1320  
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 gcagaacaga aggacagaca gcacacccta aagcatttcg agcatgtgcg catgggtggat 1500  
 cccaagaaag ccgctcagat ccggtcccag gttatgacac acctccgtgt gatttatgag 1560  
 cgcataatc agtctctctc cctgctctac aacgtgcctg cagtggccga ggagattcag 1620  
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 ccgtggcatt cttttggggc tgactctgtg ccagccaaca cagaaaacga agttgagcct 1860  
 gttgatgcc gccctgctgc cgaccgagga ctgaccactc gaccagggtc tgggttgaca 1920  
 aatatcaaga cggaggagat ctctgaagtg aagatggatg cagaattccg acatgactca 1980  
 ggatatgaag ttcacatca aaaattggtg ttctttgcag aagatgtggg ttcaaacaaa 2040  
 ggtgcaatca ttggactcat ggtgggcggt gttgtcatag cgacagtgat cgtcatcacc 2100  
 ttggtgatgc tgaagaagaa acagtacaca tccattcatc atggtgtggt ggaggttgac 2160  
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Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Ile Pro Thr Thr Ala Ala Ser Thr  
340 345 350

Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu  
355 360 365

His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg  
370 375 380

Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala Glu Arg Gln  
385 390 395 400

Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile Gln His Phe  
405 410 415

Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln  
420 425 430

Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp  
435 440 445

Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val  
450 455 460

Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg  
465 470 475 480

Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val  
485 490 495

Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met  
500 505 510

Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu  
515 520 525

Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp  
530 535 540

Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn  
545 550 555 560

Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro  
565 570 575



Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro Val Asn Gly  
580 585 590

Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp  
595 600 605

Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val Asp Ala Arg  
610 615 620

Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr  
625 630 635 640

Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe  
645 650 655

Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe  
660 665 670

Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val  
675 680 685

Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu Val Met Leu  
690 695 700

Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp  
705 710 715 720

Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn  
725 730 735

Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn Lys  
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Lys

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Gly Arg Arg Gly Ser  
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<210> 69

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Thr Gln His Gly Ile Arg  
1 5

<210> 70

<211> 6

<212> PRT

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<220>

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<400> 70

Glu Thr Asp Glu Glu Pro  
1 5

<210> 71

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

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Met Cys Ala Glu Val Lys Met Asp Ala Glu Phe Lys Asp Asn Pro  
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<210> 72

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<220>
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<400> 72

Asp Ala Glu Phe Arg
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<210> 73
<211> 5
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<220>
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<400> 73

Ser Glu Val Asn Leu
 1             5

<210> 74
<211> 4
<212> PRT
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<220>
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<220>
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<400> 74
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